~~09/967,853~~

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FULL ESTIMATED COST

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*** YOU HAVE NEW MAIL ***

=> s target and (absence or presence or amount) and specific (3a) probe?
L1 17280 TARGET AND (ABSENCE OR PRESENCE OR AMOUNT) AND SPECIFIC (3A) PROBE?

=> s l1 and no (4a) control probe?
L2 0 L1 AND NO (4A) CONTROL PROBE?

=> s l1 and control (3a) probe
L3 1174 L1 AND CONTROL (3A) PROBE

=> s l3 and substrate
L4 833 L3 AND SUBSTRATE

=> s l4 and label?
L5 810 L4 AND LABEL?

=> dup rem l5
PROCESSING IS APPROXIMATELY 88% COMPLETE FOR L5
PROCESSING COMPLETED FOR L5
L6 809 DUP REM L5 (1 DUPLICATE REMOVED)

=> s l6 and array
L7 437 L6 AND ARRAY

=> s l7 and no probe?
L8 434 L7 AND NO PROBE?

=> s l8 and (area or region or feature or portion) probe?
MISSING OPERATOR PORTION) PROBE?
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l8 and (area or region or feature or portion) (2a)probe?
L9 191 L8 AND (AREA OR REGION OR FEATURE OR PORTION) (2A) PROBE?

=> s l9 and no (3a)(area or region or feature or portion) probe?

MISSING OPERATOR PORTION) PROBE?
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l9 and no (3a)(area or region or feature or portion)(2a) probe?
L10 0 L9 AND NO (3A)(AREA OR REGION OR FEATURE OR PORTION)(2A) PROBE?

=> s l9 and no (3a)(area or region or feature or portion)(26a) probe?
L11 0 L9 AND NO (3A)(AREA OR REGION OR FEATURE OR PORTION)(26A) PROBE
?

=> s l9 and no (6a)(area or region or feature or portion)(2a) probe?
L12 0 L9 AND NO (6A)(AREA OR REGION OR FEATURE OR PORTION)(2A) PROBE?

=> s l9 and specific probe?
L13 131 L9 AND SPECIFIC PROBE?

=> s l13 and no specific probe?
L14 131 L13 AND NO SPECIFIC PROBE?

=> s l14 and py=2001
L15 20 L14 AND PY=2001

=> d l15 bib abs 1-20

L15 ANSWER 1 OF 20 USPATFULL on STN
AN 2001:237655 USPATFULL
TI Exploiting genomics in the search for new drugs
IN Lockhart, David J., Del Mar, CA, United States
Wodicka, Lisa, San Diego, CA, United States
Ho, Ming Hsiu, San Jose, CA, United States
PI US 2001055771 A1 20011227 <--
US 6524800 B2 20030225
AI US 2001-900845 A1 20010706 (9)
RLI Division of Ser. No. US 1998-215207, filed on 18 Dec 1998, UNKNOWN
DT Utility
FS APPLICATION
LREP BANNER & WITCOFF LTD.,, ATTORNEYS FOR AFFYMETRIX, 1001 G STREET , N.W.,
ELEVENTH FLOOR, WASHINGTON, DC, 20001-4597
CLMN Number of Claims: 79
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 2055
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The cellular effects of potentially therapeutic compounds are
characterized in mammalian cells and yeast. In the latter case the
effects can be characterized on a genome-wide scale by monitoring
changes in messenger RNA levels in treated cells with high-density
oligonucleotide **probe** arrays.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 2 OF 20 USPATFULL on STN
AN 2001:235088 USPATFULL
TI Exploiting genomics in the search for new drugs
IN Lockhart, David J., Del Mar, CA, United States
Wodicka, Lisa, San Diego, CA, United States
Ho, Ming Hsiu, San Jose, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6333155 B1 20011225 <--
AI US 1998-215207 19981218 (9)
PRAI US 1997-68289P 19971219 (60)

09567863

DT Utility
FS GRANTED
EXNAM Primary Examiner: Fredman, Jeffrey; Assistant Examiner: Chakrabarti, Arun Kr.
LREP Banner & Witcoff
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 1865
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The cellular effects of potentially therapeutic compounds are characterized in mammalian cells and yeast. In the latter case the effects can be characterized on a genome-wide scale by monitoring changes in messenger RNA levels in treated cells with high-density oligonucleotide **probe** arrays.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 3 OF 20 USPATFULL on STN
AN 2001:229761 USPATFULL
TI Linear **probe** carrier
IN Chen, Shiping, Rockville, MD, United States
Luo, Yuling, Castro Valley, CA, United States
PI US 2001051714 A1 20011213 <--
AI US 2001-758873 A1 20010110 (9)
PRAI US 2000-175225P 20000110 (60)
US 2000-190495P 20000320 (60)
US 2000-227874P 20000825 (60)
US 2000-244418P 20001030 (60)
DT Utility
FS APPLICATION
LREP Charles D. Holland, Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA, 94304-0792
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 15 Drawing Page(s)
LN.CNT 2203
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a **probe** carrier in which a flexible **substrate** carries a one-dimensional configuration of **probes** wherein each different type of **probe** is attached to its own discrete portion of the **substrate**. The invention also relates to a **probe** carrier in which a flexible **substrate** such as a tape or fiber carries a two-dimensional configuration of **probes**. Furthermore, systems for fabricating and packaging flexible **probe** carrier threads are presented. Flexible **probe** carrier threads are packaged in forms of pins, rods, coils and spools to increase efficiency of hybridization and generate compact formats for transportation and use of **probe** carriers. Novel methods for hybridization of packaged **probe** carriers are disclosed. Methods for reading results of hybridization to packaged **probe** carriers are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 4 OF 20 USPATFULL on STN
AN 2001:229388 USPATFULL
TI Expression monitoring of downstream genes in the BRCA1 pathway
IN Oliner, Jonathan, Mountain View, CA, United States
Christians, Fred, Los Altos, CA, United States
Truong, Vivi, San Jose, CA, United States
Haber, Daniel, Chestnut Hill, MA, United States

Bean, James, Arlington, MA, United States
Miklos, David, W. Roxbury, MA, United States
Harkin, Denis Paul, Knockhill Park, Great Britain
PI US 2001051339 A1 20011213 <--
AI US 2001-808352 A1 20010315 (9)
RLI Division of Ser. No. US 1998-203677, filed on 1 Dec 1998, GRANTED, Pat. No. US 6258536
DT Utility
FS APPLICATION
LREP BANNER & WITCOFF, 1001 G STREET N W, SUITE 1100, WASHINGTON, DC, 20001
CLMN Number of Claims: 54
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 2842
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Analysis of the genes whose expression is affected by BRCA1 has identified a set of genes, each of which is up- or down-regulated by BRCA1. Each of these genes, alone or in groups, can be used to determine the mutational status of a BRCA1 gene, to determine whether a particular allelic variant affects BRCA1 function, to diagnose neoplasia, and to help identify candidate drugs which may be useful as anti-neoplastic agents.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 5 OF 20 USPATFULL on STN
AN 2001:220859 USPATFULL
TI Electronically mediated nucleic acid amplification in NASBA
IN Edman, Carl F., San Diego, CA, United States
Nerenberg, Michael I., La Jolla, CA, United States
PA Nanogen/Becton Dickinson Partnership, San Diego, CA, United States (U.S. corporation)
PI US 6326173 B1 20011204 <--
AI US 1999-290338 19990412 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Siew, Jeffrey
LREP Lyon & Lyon LLP
CLMN Number of Claims: 64
ECL Exemplary Claim: 1
DRWN 38 Drawing Figure(s); 34 Drawing Page(s)
LN.CNT 3391
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of improving amplification of nucleic acids using a nucleic acid sequence-based amplification ("NASBA") method is provided wherein **target** nucleic acids and NASBA primers are electronically addressed to electronically addressable capture sites of a microchip. This improvement uses electronically induced hybridization of the **target** nucleic acids to the primers. The primers may be solution-based or immobilized on the capture sites of the microchip.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 6 OF 20 USPATFULL on STN
AN 2001:190911 USPATFULL
TI Multiplex amplification and separation of nucleic acid sequences on a bioelectronic microchip using asymmetric structures
IN Edman, Carl F., San Diego, CA, United States
Nerenberg, Michael I., La Jolla, CA, United States
Westin, Lorelei P., La Mesa, CA, United States
Carrino, John J., San Diego, CA, United States
PA Nanogen/Becton Dickinson Partnership, San Diego, CA, United States (U.S.

corporation)
PI US 6309833 B1 20011030 <--
AI US 1999-290452 19990412 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Lundgren, Jeffrey S.
LREP Lyon & Lyon LLP
CLMN Number of Claims: 47
ECL Exemplary Claim: 1
DRWN 38 Drawing Figure(s); 34 Drawing Page(s)
LN.CNT 3347
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for amplifying nucleic acids is provided wherein detection of amplified species is enhanced by the use of asymmetric amplification. Such amplification is made asymmetric by using divergent ratios of amplification primers or by using non-extending and/or non-cleavable amplification primers. Detection of the amplicons is improved because maintenance of single stranded species of amplicons during amplification facilitates their direct capture by immobilized **probes** without having to include denaturing steps.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 7 OF 20 USPATFULL on STN
AN 2001:190902 USPATFULL
TI Methods for analyzing a **target** nucleic acid using immobilized heterogeneous mixtures of oligonucleotide **probes**
IN Drmanac, Radoje T., Palo Alto, CA, United States
PA Hyseq, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 6309824 B1 20011030 <--
AI US 1997-784747 19970116 (8)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Myers, Carla J.
LREP Marshall, Gerstein, & Borun
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 3792
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for detecting a **target** nucleic acid species including the steps of providing an **array** of **probes** affixed to a **substrate** and a plurality of **labeled probes** wherein each **labeled probe** is selected to have a first nucleic acid sequence which is complementary to a first portion of a **target** nucleic acid and wherein the nucleic acid sequence of at least one **probe** affixed to the **substrate** is complementary to a second portion of the nucleic acid sequence of the **target**, the second portion being adjacent to the first portion; applying a **target** nucleic acid to the **array** under suitable conditions for hybridization of **probe** sequences to complementary sequences; introducing a **labeled probe** to the **array**; hybridizing a **probe** affixed to the **substrate** to the **target** nucleic acid; hybridizing the **labeled probe** to the **target** nucleic acid; affixing the **labeled probe** to an adjacently hybridized **probe** in the **array**; and detecting the **labeled probe** affixed to the **probe** in the **array**.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 8 OF 20 USPATFULL on STN
AN 2001:190900 USPATFULL
TI Method for comparing copy number of nucleic acid sequences
IN Fodor, Stephen P. A., Palo Alto, CA, United States
Solas, Dennis W., San Francisco, CA, United States
Dower, William J., Menlo Park, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6309822 B1 20011030 <--
AI US 1996-772376 19961223 (8)
RLI Continuation-in-part of Ser. No. US 1990-670118, filed on 25 Jun 1990, now patented, Pat. No. US 5800992 Continuation-in-part of Ser. No. US 1999-529115, filed on 15 Sep 1999, now patented, Pat. No. US 6040138 Division of Ser. No. US 1993-168904, filed on 15 Dec 1993, now abandoned Continuation of Ser. No. US 1990-624114, filed on 6 Dec 1990, now abandoned Continuation-in-part of Ser. No. US 1989-362901, filed on 7 Jun 1989, now abandoned
PRAI WO 1996-US14839 19960913
DT Utility
FS GRANTED
EXNAM Primary Examiner: Zitomer, Stephanie
LREP Pillsbury Winthrop LLP
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 7686
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides methods for comparing and identifying differences in nucleic acid sequences using a plurality of sequence specific recognition reagents (i.e., **probes** comprising a nucleic acid complementary to a nucleic acid sequence in collections to be compared) bound to a solid surface.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 9 OF 20 USPATFULL on STN
AN 2001:178805 USPATFULL
TI Expression monitoring for gene function identification
IN Mack, David H., Menlo Park, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6303301 B1 20011016 <--
AI US 1998-86285 19980529 (9)
RLI Continuation-in-part of Ser. No. WO 1998-US1206, filed on 12 Jan 1998
PRAI US 1997-35327P 19970113 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Forman, B J.
LREP Banner & Witcoff, Ltd.
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 24 Drawing Figure(s); 21 Drawing Page(s)
LN.CNT 2680
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides methods, compositions and apparatus for mapping the regulatory relationship among genes by massive parallel monitoring gene expression. In some embodiments, mutations in the up-stream regulatory genes are detected by monitoring the change in down-stream gene expression. Similarly, the function of a specific mutation in a up-stream gene is determined by monitoring the down-stream gene expression. In addition, regulatory function of a **target** gene can be determined by monitoring the expression of a large number of down-stream genes. The invention also provides specific embodiments for

detecting p53 functional homozygous and heterozygous mutations and for determining the function of p53 mutations.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 10 OF 20 USPATFULL on STN
AN 2001:173319 USPATFULL
TI Method for measuring messenger RNA
IN Akitaya, Tatsuo, Takasuzu, Japan
Mitsuhashi, Masato, Irvine, CA, United States
Cooper, Allan, Bellview, WA, United States
PA Hitachi Chemical Research Center, Inc., Irvine, CA, United States (U.S. corporation)
Hitachi Chemical Company, Ltd., Tokyo, Japan (non-U.S. corporation)
PI US 6300058 B1 20011009 <--
AI US 1992-974409 19921112 (7)
RLI Continuation-in-part of Ser. No. US 1992-857059, filed on 24 Mar 1992, now abandoned Continuation-in-part of Ser. No. US 1992-827208, filed on 29 Jan 1992, now abandoned Continuation-in-part of Ser. No. US 1992-827975, filed on 29 Jan 1992, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Guzo, David
LREP Knobbe, Martens, Olsen & Bear, LLP
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 71 Drawing Figure(s); 68 Drawing Page(s)
LN.CNT 3972
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for detecting and quantifying mRNA in a sample. The mRNA that can be detected has a unique sequence. The method includes immobilizing a first polynucleotide to an insoluble support. The first polynucleotide has a first sequence that hybridizes to the unique sequence on the mRNA. After immobilization of the first polynucleotide, the sample is applied to the insoluble support under conditions that allow the unique sequence on the mRNA to hybridize with the first polynucleotide. Thereafter, a second polynucleotide is applied to the insoluble support. This second polynucleotide has a second sequence thereon that hybridizes to a portion of the mRNA other than the unique sequence. The application of the second polynucleotide is performed under conditions that allow the second polynucleotide to hybridize with mRNA immobilized on said support, if present. Finally, the **amount** of the second polynucleotide immobilized on the support is measured to provide an indication of the **amount** of mRNA present in the sample. Polynucleotide immobilized supports and sequences useful in the method are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 11 OF 20 USPATFULL on STN
AN 2001:167894 USPATFULL
TI Methods for sequencing repetitive sequences and for determining the order of sequence subfragments
IN Drmanac, Radoje T., Palo Alto, CA, United States
Drmanac, Snezana, Palo Alto, CA, United States
Hou, Aaron, San Mateo, CA, United States
Hauser, Brian, Campbell, CA, United States
PA Hyseq, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 6297006 B1 20011002 <--
AI US 1997-812951 19970304 (8)
RLI Continuation-in-part of Ser. No. US 1997-784747, filed on 16 Jan 1997
DT Utility

09567863

FS GRANTED
EXNAM Primary Examiner: Myers, Carla J.
LREP Marshall, Gerstein & Borun
CLMN Number of Claims: 3
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 3908
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for detecting a **target** nucleic acid species including the steps of providing an **array** of **probes** affixed to a **substrate** and a plurality of **labeled probes** wherein each **labeled probe** is selected to have a first nucleic acid sequence which is complementary to a first portion of a **target** nucleic acid and wherein the nucleic acid sequence of at least one **probe** affixed to the **substrate** is complementary to a second portion of the nucleic acid sequence of the **target**, the second portion being adjacent to the first portion; applying a **target** nucleic acid to the **array** under suitable conditions for hybridization of **probe** sequences to complementary sequences; introducing a **labeled probe** to the **array**; hybridizing a **probe** affixed to the **substrate** to the **target** nucleic acid; hybridizing the **labeled probe** to the **target** nucleic acid; affixing the **labeled probe** to an adjacently hybridized **probe** in the **array**; and detecting the **labeled probe** affixed to the **probe** in the **array**.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 12 OF 20 USPATFULL on STN
AN 2001:152686 USPATFULL
TI Allele detection using primer extension with sequence-coded identity tags
IN Huang, Xiaohua, Mountain View, CA, United States
Ryder, Tom, Los Gatos, CA, United States
Kaplan, Paul, Campbell, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6287778 B1 20010911 <--
AI US 1999-420805 19991019 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Taylor, Janell E.
LREP Banner & Witcoff, Ltd.
CLMN Number of Claims: 72
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 1380
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for determining the genotype of one or more individuals at a polymorphic locus employs amplification of a region of DNA, **labeling** of allele-specific extension primers containing tags, and hybridization of the products to an **array** of **probes**. The genotype is identified from the pattern of hybridization. The method can also be used to determine the frequency of different alleles in a population.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 13 OF 20 USPATFULL on STN
AN 2001:145503 USPATFULL
TI Method and system for providing a **probe array** chip

design database
IN Balaban, David, San Jose, CA, United States
Hubbell, Earl, Los Angeles, CA, United States
Mittman, Michael, Palo Alto, CA, United States
Cheung, Gloria, Cupertino, CA, United States
Dai, Josie, San Jose, CA, United States
PI US 2001018642 A1 20010830 <--
AI US 2001-737838 A1 20010326 (9)
RLI Continuation of Ser. No. US 1998-122304, filed on 24 Jul 1998, GRANTED, Pat. No. US 6188783
PRAI US 1997-53842P 19970725 (60)
US 1997-69198P 19971211 (60)
US 1997-69436P 19971211 (60)
DT Utility
FS APPLICATION
LREP TOWNSEND AND TOWNSEND AND CREW, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 10 Drawing Page(s)
LN.CNT 1158
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Systems and method for organizing information relating to the design of polymer **probe array** chips including oligonucleotide **array** chips. A database model is provided which organizes information interrelating **probes** on a chip, genomic items investigated by the chip, and sequence information relating to the design of the chip. The model is readily translatable into database languages such as SQL. The database model scales to permit storage of information about large numbers of chips having complex designs.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 14 OF 20 USPATFULL on STN
AN 2001:107621 USPATFULL
TI Expression monitoring of downstream genes in the BRCA1 pathway
IN Oliner, Jonathan, 173 Sierra Vista Ave., Unit 22, Mountain View, CA, United States 94043
Christians, Fred, 1444 Arbor Ave., Los Altos, CA, United States 94024
Truong, Vivi, 7082 Kindra Hill Dr., San Jose, CA, United States 95120
Haber, Daniel, 34 Monadonck Rd., Chestnut Hill, MA, United States 02467
Bean, James, 9 Heath Rd., Arlington, MA, United States 02474
Miklos, David, 61 Oriole St., W. Roxbury, MA, United States 02132
Harkin, Denis Paul, 9 Knockhill Park, Belfast BT5 6HX, Northern Ireland, United Kingdom
PI US 6258536 B1 20010710 <--
AI US 1998-203677 19981201 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Fredman, Jeffrey; Assistant Examiner: Chakrabarti, Arun K.
LREP Banner & Witcoff, Ltd.
CLMN Number of Claims: 32
ECL Exemplary Claim: 1
DRWN 24 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 2762
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Analysis of the genes whose expression is affected by BRCA1 has identified a set of genes, each of which is up- or down-regulated by BRCA1. Each of these genes, alone or in groups, can be used to determine the mutational status of a BRCA1 gene, to determine whether a particular allelic variant affects BRCA1 function, to diagnose neoplasia, and to

help identify candidate drugs which may be useful as anti-neoplastic agents.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 15 OF 20 USPATFULL on STN
AN 2001:78896 USPATFULL
TI High throughput assay system
IN Kris, Richard M, Tucson, AZ, United States
Felder, Stephen, Tucson, AZ, United States
PA High Throughput Genomics, Inc., Tucson, AZ, United States (U.S. corporation)
PI US 6238869 B1 20010529 <--
AI US 1999-337325 19990621 (9)
RLI Continuation-in-part of Ser. No. US 1998-218166, filed on 22 Dec 1998, now abandoned
PRAI US 1997-68291P 19971219 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Kim, Young
LREP Millen, White, Zelano & Branigan
CLMN Number of Claims: 32
ECL Exemplary Claim: 1
DRWN 28 Drawing Figure(s); 22 Drawing Page(s)
LN.CNT 3409
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to compositions, apparatus and methods useful for concurrently performing multiple, high throughput, biological or chemical assays, using repeated arrays of **probes**. A combination of the invention comprises a surface, which comprises a plurality of test regions, at least two of which, and in a preferred embodiment, at least twenty of which, are substantially identical, wherein each of the test regions comprises an **array** of generic anchor molecules. The anchors are associated with bifunctional linker molecules, each containing a portion which is specific for at least one of the anchors and a portion which is a **probe specific** for a **target** of interest. The resulting **array** of **probes** is used to analyze the **presence** or test the activity of one or more **target** molecules which specifically interact with the **probes**. In one embodiment of the invention, the test regions (which can be wells) are further subdivided into smaller subregions (indentations, or dimples).

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 16 OF 20 USPATFULL on STN
AN 2001:78895 USPATFULL
TI Multiplex amplification and separation of nucleic acid sequences using ligation-dependant strand displacement amplification and bioelectronic chip technology
IN Carrino, John J., San Diego, CA, United States
Gerrue, Louis O., San Diego, CA, United States
Diver, Jonathan M., San Diego, CA, United States
PA Nanogen/Becton Dickinson Partnership, San Diego, CA, United States (U.S. corporation)
PI US 6238868 B1 20010529 <--
AI US 1999-290577 19990412 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Taylor, Janell
LREP Lyon & Lyon LLP
CLMN Number of Claims: 43

09567863

ECL Exemplary Claim: 1
DRWN 38 Drawing Figure(s); 34 Drawing Page(s)
LN.CNT 3301
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to devices, methods, and compositions of matter for the multiplex amplification and analysis of nucleic acid sequences in a sample using ligation-dependent strand displacement amplification technologies in combination with bioelectronic microchip technology.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 17 OF 20 USPATFULL on STN
AN 2001:71301 USPATFULL
TI High throughput assay system
IN Felder, Stephen, Tucson, AZ, United States
Kris, Richard M., Tucson, AZ, United States
PA NeoGen, Inc., Tucson, AZ, United States (U.S. corporation)
PI US 6232066 B1 20010515 <--
AI US 1998-109076 19980702 (9)
PRAI US 1997-68291P 19971219 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Millen, White, Zelano, Branigan, P.C.
CLMN Number of Claims: 41
ECL Exemplary Claim: 1
DRWN 30 Drawing Figure(s); 25 Drawing Page(s)
LN.CNT 2577
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to compositions, apparatus and methods useful for concurrently performing multiple, high throughput, biological or chemical assays, using repeated arrays of **probes**. A combination of the invention comprises a surface, which comprises a plurality of test regions, at least two of which, and in a preferred embodiment, at least twenty of which, are substantially identical, wherein each of the test regions comprises an **array** of generic anchor molecules. The anchors are associated with bifunctional linker molecules, each containing a portion which is specific for at least one of the anchors and a portion which is a **probe specific** for a **target** of interest. The resulting **array** of **probes** is used to analyze the **presence** or test the activity of one or more **target** molecules which specifically interact with the **probes**. In one embodiment of the invention, the test regions (which can be wells) are further subdivided into smaller subregions (indentations, or dimples).

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 18 OF 20 USPATFULL on STN
AN 2001:29302 USPATFULL
TI **Target**-dependent reactions using structure-bridging oligonucleotides
IN Neri, Bruce, Madison, WI, United States
Dong, Fang, Madison, WI, United States
Lyamichev, Victor, Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
Fors, Lance, Monrovia, CA, United States
PA Third Wave Technologies, Inc., Madison, WI, United States (U.S. corporation)
PI US 6194149 B1 20010227 <--
AI US 1998-34205 19980303 (9)
DT Utility

09567863

FS Granted
EXNAM Primary Examiner: Whisenant, Ethan
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 50 Drawing Figure(s); 50 Drawing Page(s)
LN.CNT 4770
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to methods and compositions for analyzing nucleic acids. In particular, the present invention provides methods and compositions for the detection and characterization of nucleic acid sequences and sequence changes. The methods of the present invention permit the detection and/or identification of genetic polymorphism such as those associated with human disease and permit the identification of pathogens (e.g., viral and bacterial strain identification).

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 19 OF 20 USPATFULL on STN
AN 2001:23225 USPATFULL
TI Method and system for providing a **probe array** chip design database
IN Balaban, David J., San Rafael, CA, United States
Hubbell, Earl A., Los Angeles, CA, United States
Mittmann, Michael P., Palo Alto, CA, United States
Cheung, Gloria, Cupertino, CA, United States
Dai, Josie, San Jose, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6188783 B1 20010213 <--
AI US 1998-122304 19980724 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Bella, Matthew C.; Assistant Examiner: Choobin, M.
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1021
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Systems and method for organizing information relating to the design of polymer **probe array** chips including oligonucleotide **array** chips. A database model is provided which organizes information interrelating **probes** on a chip, genomic items investigated by the chip, and sequence information relating to the design of the chip. The model is readily translatable into database languages such as SQL. The database model scales to permit storage of information about large numbers of chips having complex designs.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L15 ANSWER 20 OF 20 USPATFULL on STN
AN 2001:10710 USPATFULL
TI Downstream genes of tumor suppressor WT1
IN Oliner, Jonathan, Mountain View, CA, United States
Truong, Vivi, San Jose, CA, United States
Haber, Daniel, Chestnut Hill, MA, United States
Lee, Sean, Malden, MA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6177248 B1 20010123 <--
AI US 1999-256301 19990224 (9)
DT Utility
FS Granted

09567863

EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Siu, Stephen
LREP Banner & Witcoff Ltd.
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1593
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for diagnosing cancers, drug-screening, and functionally analyzing mutations involving the WT1 gene. The methods involve use of the newly identified set of genes which are regulated by WT1 as well as by the set of genes which are regulated by WT1 fusions to EWS. Monitoring expression levels of these sets of genes can be used as an indicator of the genetic status of the gene. It can also identify which have similar effects on down-stream genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

09567863

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=> s competiti? hybridization?/ti
L27         112 COMPETITI? HYBRIDIZATION?/TI

=> s l27 and py=2001
L28          12 L27 AND PY=2001

=> dup rem l28
PROCESSING COMPLETED FOR L28
L29           7 DUP REM L28 (5 DUPLICATES REMOVED)

=> d l29 bib abs 1-7

L29  ANSWER 1 OF 7  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 1
AN   2001:453321  BIOSIS
DN   PREV200100453321
TI   Kit for detecting nucleic acid sequences using competitive
     hybridization probes.
AU   Lucas, Joe N. [Inventor]; Straume, Tore [Inventor, Reprint author]; Bogen,
     Kenneth T. [Inventor]
CS   Tracy, CA, USA
     ASSIGNEE: The Regents of the University of California
PI   US 6270972 August 07, 2001
SO   Official Gazette of the United States Patent and Trademark Office Patents,
     (Aug. 7, 2001) Vol. 1249, No. 1. e-file.
     CODEN: OGUPE7. ISSN: 0098-1133.
DT   Patent
LA   English
ED   Entered STN: 26 Sep 2001
     Last Updated on STN: 22 Feb 2002
AB   A kit is provided for detecting a target nucleic acid sequence in a
     sample, the kit comprising: a first hybridization probe which includes a
     nucleic acid sequence that is sufficiently complementary to selectively
     hybridize to a first portion of the target sequence, the first
     hybridization probe including a first complexing agent for forming a
     binding pair with a second complexing agent; and a second hybridization
     probe which includes a nucleic acid sequence that is sufficiently
     complementary to selectively hybridize to a second portion of the target
     sequence to which the first hybridization probe does not selectively
     hybridize, the second hybridization probe including a detectable marker; a
     third hybridization probe which includes a nucleic acid sequence that is
     sufficiently complementary to selectively hybridize to a first portion of
     the target sequence, the third hybridization probe including the same
     detectable marker as the second hybridization probe; and a fourth
     hybridization probe which includes a nucleic acid sequence that is
     sufficiently complementary to selectively hybridize to a second portion of
     the target sequence to which the third hybridization probe does not
     selectively hybridize, the fourth hybridization probe including the first
     complexing agent for forming a binding pair with the second complexing
     agent; wherein the first and second hybridization probes are capable of
     simultaneously hybridizing to the target sequence and the third and fourth
     hybridization probes are capable of simultaneously hybridizing to the
     target sequence, the detectable marker is not present on the first or
     fourth hybridization probes and the first, second, third, and fourth
     hybridization probes each include a competitive nucleic acid sequence
     which is sufficiently complementary to a third portion of the target
     sequence that the competitive sequences of the first, second, third, and
     fourth hybridization probes compete with each other to hybridize to the
     third portion of the target sequence.
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L29 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
AN 2001:886549 CAPLUS
DN 136:1601
TI Identification of nucleotide sequence polymorphisms with **competitive hybridization** and fluorimetric detection for use in genetic analysis
IN Poetter, Karl; Foote, Simon
PA The Walter and Eliza Hall Institute of Medical Research, Australia
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001092564	A1	20011206	WO 2001-AU635	20010529 <--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 760403	B2	20030515	AU 2001-61906	20010529
	NZ 516930	A	20030926	NZ 2001-516930	20010529
	US 2004014065	A1	20040122	US 2003-296860	20030519
PRAI	AU 2000-7811	A	20000529		
	WO 2001-AU635	W	20010529		

AB The present invention relates generally is a method for determining the likelihood that a test polynucleotide sequence differs from a driver polynucleotide sequence. More particularly, the present method uses fluorescence-based technol. in the assessment of the results of competitive hybridization between polynucleotide sequences. The present method does not require nucleotide sequencing or gel electrophoresis and is capable of being multiplexed and automated. The methods of the present invention will find broad application in the anal. of polynucleotides, inter alia in genetic anal., specific locus testing, genotyping, mutation detection, the discovery and detection of single nucleotide polymorphisms (SNPs) and mapping.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L29 ANSWER 3 OF 7 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
AN 2001-211231 [21] WPIDS
DNN N2001-150886 DNC C2001-062821
TI Detection and quantitation of variation or polymorphism of genes in specimens for distinguishing and identifying nucleic acid in e.g. diagnosis and treatment of cancer by **competitive hybridization**.
DC B04 D16 S03
IN YAMANE, A
PA (WAKT) WAKUNAGA PHARM CO LTD; (WAKT) WAKUNAGA SEIYAKU KK
CYC 94
PI WO 2001012849 A1 20010222 (200121)* JA 47p <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

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AU 2000063204 A 20010313 (200134) <--
JP 2001516936 X 20030311 (200319)
JP 2003174882 A 20030624 (200351) 16p
ADT WO 2001012849 A1 WO 2000-JP5286 20000807; AU 2000063204 A AU 2000-63204 20000807; JP 2001516936 X WO 2000-JP5286 20000807, JP 2001-516936 20000807; JP 2003174882 A JP 1999-228163 19990812
FDT AU 2000063204 A Based on WO 2001012849; JP 2001516936 X Based on WO 2001012849
PRAI JP 1999-228163 19990812
AN 2001-211231 [21] WPIDS
AB WO 200112849 A UPAB: 20010418
NOVELTY - Distinguishing the homogeneity of a mixture of first and second nucleic acids performed by competitive hybridization is new.

DETAILED DESCRIPTION - In the method at least 2 labels capable of mutually transferring energy are introduced into 3'-terminus of the first double-stranded nucleic acid and 5'-terminus of the other chain for labeling before the hybridization with the non-labeled second nucleic acid, measuring the extent of energy change caused by the energy transfer between the labels in association with the complementary strand substitution, and evaluating the extent of such substitution between these nucleic acids.

INDEPENDENT CLAIMS are also included for:

(1) a similar method in which both the first and second nucleic acid are labeled in the 3'- or/and 5'-termini with the labels in various combinations prior to hybridization; and

(2) a kit for use in the method containing reagents for nucleic acid amplification of a specific domain in a sequence, reagents for distinguishing homogeneity of the target nucleic acid by comparing with a standard, and reagents for labeling and subsequent procedures.

USE - The method is for distinguishing and identifying nucleic acid in diagnosis and treatment of cancer, specific viral and bacterial infections, and judging success as well as degree of rejection of bone marrow treatment.

ADVANTAGE - Such method is direct, rapid and accurate, without needing solid-liquid separation to simplify the procedure.

DESCRIPTION OF DRAWING(S) - A diagram showing the method for distinguishing nucleic acids: (a) normal nucleic acids; and (b) mutated nucleic acids.

Dwg.1/4

L29 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 2001:504448 BIOSIS
DN PREV200100504448
TI Characterization of an ethylene-induced esterase gene isolated from Citrus sinensis by **competitive hybridization**.
AU Zhong, Guang Yan; Goren, Raphael; Riov, Joseph; Sisler, Edward C.; Holland, Doron [Reprint author]
CS Newe Ya'ar Research Center, Agricultural Research Organization, Ramat Yishay, 30095, Israel
vhhollan@agri.gov.il
SO Physiologia Plantarum, (October, 2001) Vol. 113, No. 2, pp. 267-274. print.
CODEN: PHPLAI. ISSN: 0031-9317.
DT Article
LA English
ED Entered STN: 31 Oct 2001
Last Updated on STN: 23 Feb 2002
AB A simple new method, competitive hybridization, for identification of differentially regulated genes was used to isolate novel genes induced by ethylene in citrus (Citrus sinensis (L.) Osbeck cv. Shamouti) leaves. One of the isolated genes, an ethylene-induced esterase gene (EIE), was

further characterized. The deduced protein sequence of this gene shows a similarity to those of several plant alpha/beta hydrolase gene family members, which are known to be involved in secondary metabolism. Northern blot analysis demonstrated that EIE mRNA was induced by ethylene within 4 h and accumulated to a very high level 24 h after the initiation of ethylene treatment. Induction of EIE by ethylene could be counteracted by 1-methylcyclopropene, a potent ethylene perception inhibitor, indicating that the expression of EIE is ethylene-dependent. The bacterially expressed protein of EIE was recognized by antiserum against Pir7b, a naphthol AS esterase induced in rice by the non-host pathogen, Pseudomonas syringae pv. syringae. The EIE protein was identified in ethylene-treated leaves using anti-Pir7b antibodies. An alpha-naphthyl acetate esterase accumulated concomitantly with the increase in EIE protein in ethylene-treated citrus leaves. An enzyme activity assay followed by western analysis confirmed that the esterase was EIE.

L29 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:543047 BIOSIS
DN PREV200100543047
TI Novel HCV genotyping assay by microwell plate amplification and **competitive hybridization**: HCV-G-MACH assay.
AU Mukaide, Motokazu [Reprint author]; Yoshioka, Kentaro; Kaufmann, Gilbert R.; Suzuki, Kazuo; Fujise, Kiyotaka; Hayashida, Kazuhiro; Imai, Mitsunobu; Kakuda, Hirokazu; Saito, Yumiko; Kelleher, Anthony; Cooper, David A.; Kakumu, Shinichi
CS SRL, Inc, Tokyo, Japan
SO Hepatology, (October, 2001) Vol. 34, No. 4 Pt. 2, pp. 229A. print.
Meeting Info.: 52nd Annual Meeting and Postgraduate Courses of the American Association for the Study of Liver Diseases. Dallas, Texas, USA. November 09-13, 2001.
CODEN: HPTLD9. ISSN: 0270-9139.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 21 Nov 2001
Last Updated on STN: 25 Feb 2002

L29 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
AN 1999:454271 CAPLUS
DN 131:83965
TI Solid phase selection of differentially expressed genes by **competitive hybridization** with reference DNA cloned on microparticles
IN Albrecht, Glen; Brenner, Sydney; Dubridge, Robert
PA Lynx Therapeutics, Inc., USA
SO PCT Int. Appl., 108 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9935293	A2	19990715	WO 1999-US666	19990108
	WO 9935293	A3	19990930		

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,

CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

	US 6265163	B1	20010724	US 1998-130546	19980806 <--
	CA 2317695	AA	19990715	CA 1999-2317695	19990108
	AU 9921139	A1	19990726	AU 1999-21139	19990108
	AU 754929	B2	20021128		
	EP 1054999	A2	20001129	EP 1999-901448	19990108
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2002500050	T2	20020108	JP 2000-527674	19990108
	NO 2000003531	A	20000905	NO 2000-3531	20000707
PRAI	US 1998-5222	A	19980109		
	US 1998-130546	A	19980806		
	WO 1999-US666	W	19990108		

AB The invention provides a method and materials for monitoring and isolating differentially expressed genes. In accordance with the method of the invention, differently labeled populations of DNAs from sources to be compared are competitively hybridized with reference DNA cloned on solid phase supports, e.g. microparticles, to provide a differential expression library which, in the preferred embodiment, may be manipulated by fluorescence-activated cell sorting (FACS). Monitoring the relative signal intensity of the different fluorescent labels on the microparticles permits quant. anal. of expression levels relative to the reference DNA. The invention also provides a method for identifying and isolating rare genes. Populations of microparticles having relative signal intensities of interest can be isolated by FACS and the attached DNAs identified by sequencing, such as with massively parallel signature sequencing (MPSS), or with conventional DNA sequencing protocols.

L29 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:231442 CAPLUS
DN 126:247542
TI Detection and isolation of nucleic acid sequences using **competitive hybridization** probes
IN Lucas, Joe N.; Straume, Tore; Bogen, Kenneth T.
PA Regents of the University of California, USA
SO U.S., 10 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5616465	A	19970401	US 1995-512897	19950809
	US 6270972	B1	20010807	US 1999-364155	19990730 <--
PRAI	US 1995-512897	A1	19950809		
	US 1996-720540	A1	19960930		

AB A method for detecting a target nucleic acid sequence in a sample is provided using hybridization probes which competitively hybridize to a target nucleic acid. A target nucleic acid sequence is hybridized to first and second hybridization probes which are complementary to overlapping portions of the target nucleic acid sequence, the first hybridization probe including a first complexing agent capable of forming a binding pair with a second complexing agent and the second hybridization probe including a detectable marker. The first complexing agent attached to the first hybridization probe is contacted with a second complexing agent, the second complexing agent being attached to a solid support such that when the first and second complexing agents are attached, target nucleic acid sequences hybridized to the first hybridization probe become immobilized on to the solid support. The immobilized target nucleic acids are then separated and detected by detecting the detectable marker attached to the second hybridization probe. A kit for performing the method is also provided.

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=> s l29 and array
L30           0 L29 AND ARRAY

=> s l29 and substrate
L31           0 L29 AND SUBSTRATE

=> s l29 and surface
L32           0 L29 AND SURFACE

=> d
L32 HAS NO ANSWERS
L27         112 SEA COMPETITI? HYBRIDIZATION?/TI
L28          12 SEA L27 AND PY=2001
L29           7 DUP REM L28 (5 DUPLICATES REMOVED)
L32           0 SEA L29 AND SURFACE


=> s s competiti? hybridizztion and array
<------User Break------>

SEARCH ENDED BY USER
SEARCH ENDED BY USER

=> s competit? hybridization and array
L33         199 COMPETIT? HYBRIDIZATION AND ARRAY

=> s l33 and label? probe and label? target
L34          37 L33 AND LABEL? PROBE AND LABEL? TARGET

=> dup rem l34
PROCESSING COMPLETED FOR L34
L35          37 DUP REM L34 (0 DUPLICATES REMOVED)

=> s l35 and py=2001
L36           4 L35 AND PY=2001

=> d l36 bib abs 1-4

L36  ANSWER 1 OF 4  USPATFULL on STN
AN     2001:190902  USPATFULL
TI     Methods for analyzing a target nucleic acid using immobilized
       heterogeneous mixtures of oligonucleotide probes
IN     Drmanac, Radoje T., Palo Alto, CA, United States
PA     Hyseq, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI     US 6309824          B1   20011030                                <--
AI     US 1997-784747           19970116 (8)
DT     Utility
FS     GRANTED
EXNAM  Primary Examiner: Myers, Carla J.
LREP   Marshall, Gerstein, & Borun
CLMN   Number of Claims: 18
ECL    Exemplary Claim: 1
DRWN   No Drawings
LN.CNT 3792
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The present invention provides a method for detecting a target nucleic
       acid species including the steps of providing an array of
       probes affixed to a substrate and a plurality of labeled probes wherein
       each labeled probe is selected to have a first
       nucleic acid sequence which is complementary to a first portion of a
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target nucleic acid and wherein the nucleic acid sequence of at least one probe affixed to the substrate is complementary to a second portion of the nucleic acid sequence of the target, the second portion being adjacent to the first portion; applying a target nucleic acid to the **array** under suitable conditions for hybridization of probe sequences to complementary sequences; introducing a **labeled probe** to the **array**; hybridizing a probe affixed to the substrate to the target nucleic acid; hybridizing the **labeled probe** to the target nucleic acid; affixing the **labeled probe** to an adjacently hybridized probe in the **array**; and detecting the **labeled probe** affixed to the probe in the **array**.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L36 ANSWER 2 OF 4 USPATFULL on STN
AN 2001:167894 USPATFULL
TI Methods for sequencing repetitive sequences and for determining the order of sequence subfragments
IN Drmanac, Radoje T., Palo Alto, CA, United States
Drmanac, Snezana, Palo Alto, CA, United States
Hou, Aaron, San Mateo, CA, United States
Hauser, Brian, Campbell, CA, United States
PA Hyseq, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 6297006 B1 20011002 <--
AI US 1997-812951 19970304 (8)
RLI Continuation-in-part of Ser. No. US 1997-784747, filed on 16 Jan 1997
DT Utility
FS GRANTED
EXNAM Primary Examiner: Myers, Carla J.
LREP Marshall, Gerstein & Borun
CLMN Number of Claims: 3
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 3908
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for detecting a target nucleic acid species including the steps of providing an **array** of probes affixed to a substrate and a plurality of labeled probes wherein each **labeled probe** is selected to have a first nucleic acid sequence which is complementary to a first portion of a target nucleic acid and wherein the nucleic acid sequence of at least one probe affixed to the substrate is complementary to a second portion of the nucleic acid sequence of the target, the second portion being adjacent to the first portion; applying a target nucleic acid to the **array** under suitable conditions for hybridization of probe sequences to complementary sequences; introducing a **labeled probe** to the **array**; hybridizing a probe affixed to the substrate to the target nucleic acid; hybridizing the **labeled probe** to the target nucleic acid; affixing the **labeled probe** to an adjacently hybridized probe in the **array**; and detecting the **labeled probe** affixed to the probe in the **array**.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L36 ANSWER 3 OF 4 USPATFULL on STN
AN 2001:125734 USPATFULL
TI Methods and apparatus for DNA sequencing and DNA identification
IN Drmanac, Radoje, Sunnyvale, CA, United States
PA Hyseq, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 6270961 B1 20010807 <--

09567863

AI US 1994-353554 19941209 (8)
RLI Continuation-in-part of Ser. No. US 1994-203502, filed on 28 Feb 1994, now patented, Pat. No. US 5525464 Continuation of Ser. No. US 1993-48152, filed on 15 Apr 1993, now abandoned Continuation of Ser. No. US 1990-576559, filed on 31 Aug 1990, now abandoned Continuation-in-part of Ser. No. US 1988-175088, filed on 30 Mar 1988, now abandoned
PRAI YU 1987-570 19870419
YU 1987-570 19870918
DT Utility
FS GRANTED
EXNAM Primary Examiner: Fredman, Jeffrey
LREP Marshall, O'Toole, Gerstein, Murray & Borun
CLMN Number of Claims: 37
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 2348
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Sequencing by Hybridization (SBH) methods and apparatus employing subdivided filters for discrete multiple probe analysis of multiple samples may be used for DNA identification and for DNA sequencing. Partitioned filters are prepared. Samples are affixed to sections of partitioned filters and each sector is probed with a single probe or a multiplexed probe for hybridization scoring. Hybridization data is analyzed for probe complementarity, partial sequencing by SBH or complete sequencing by SBH.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L36 ANSWER 4 OF 4 USPATFULL on STN
AN 2001:109862 USPATFULL
TI METHODS OF ASSAYING DIFFERENTIAL EXPRESSION
IN CHENCHIK, ALEX, PALO ALTO, CA, United States
JOKHADZE, GEORGE, MOUNTAIN VIEW, CA, United States
BIBILASHVILLI, ROBERT, MOSCOW, Russian Federation
PI US 2001007744 A1 20010712 <--
US 6489455 B2 20021203
AI US 1999-225201 A1 19990105 (9)
DT Utility
FS APPLICATION
LREP BRET E FIELD, BOZICEVIC, FIELD & FRANCIS LLP, 200 MIDDLEFIELD ROAD, SUITE 200, MENLO PARK, CA, 94025
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1134
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions are provided for analyzing differences in the RNA profiles between a plurality of different physiological samples. In the subject methods, a set of a representational number of distinct gene specific primers is used to generate labeled nucleic acids from each of the different physiological samples. The labeled nucleic acids are then compared to each other and differences in the RNA profiles are determined. The subject methods find use in methods of identifying differential gene expression.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.